

R. Mitra

# 8  
RSL Entered 1653  
7/5/01RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/523,647DATE: 07/05/2001  
TIME: 11:21:32Input Set : A:\32931227.app  
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3 <110> APPLICANT: MURDIN, ANDREW D.  
 4 OOMEN, RAYMOND P.  
 5 WANG, JOE  
 6 DUNN, PAMELA  
 8 <120> TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING  
 9 DNA FRAGMENTS AND USES THEREOF  
 11 <130> FILE REFERENCE: 032931/0227  
 13 <140> CURRENT APPLICATION NUMBER: 09/523,647  
 C--> 14 <141> CURRENT FILING DATE: 2000-03-10  
 16 <150> PRIOR APPLICATION NUMBER: 60/123,966  
 17 <151> PRIOR FILING DATE: 1999-03-12  
 19 <160> NUMBER OF SEQ ID NOS: 4  
 21 <170> SOFTWARE: PatentIn Ver. 2.1  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 2111  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Chlamydia pneumoniae  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: CDS  
 30 <222> LOCATION: (139)..(1809)  
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 37 atgcgtatagg agatccct atg tcc aaa ctc atc aga cga gta gtt acg gtc 171  
 38 Met Ser Lys Leu Ile Arg Arg Val Val Thr Val  
 39 1 5 10  
 41 ctt gcg cta acg agt atg gcg agt tgc ttt gcc agc ggg ggt ata gag 219  
 42 Leu Ala Leu Thr Ser Met Ala Ser Cys Phe Ala Ser Gly Gly Ile Glu  
 43 15 20 25  
 45 gcc gct gta gca gag tct ctg att act aag atc gtc gct agt gcg gaa 267  
 46 Ala Ala Val Ala Glu Ser Leu Ile Thr Lys Ile Val Ala Ser Ala Glu  
 47 30 35 40  
 49 aca aag cca gca cct gtt cct atg aca gcg aag aag gtt aga ctt gtc 315  
 50 Thr Lys Pro Ala Pro Val Pro Met Thr Ala Lys Lys Val Arg Leu Val  
 51 45 50 55  
 53 cgt aga aat aaa caa cca gtt gaa caa aaa agc cgt ggt gct ttt tgt 363  
 54 Arg Arg Asn Lys Gln Pro Val Glu Gln Lys Ser Arg Gly Ala Phe Cys  
 55 60 65 70 75  
 57 gat aaa gaa ttt tat ccc tgt gaa gag gga cga tgt caa cct gta gag 411  
 58 Asp Lys Glu Phe Tyr Pro Cys Glu Glu Gly Arg Cys Gln Pro Val Glu  
 59 80 85 90  
 61 gct cag caa gag tct tgc tac gga aga ttg tat tct gta aaa gta aac 459  
 62 Ala Gln Gln Glu Ser Cys Tyr Gly Arg Leu Tyr Ser Val Lys Val Asn  
 63 95 100 105  
 65 gat gat tgc aac gta gaa att tgc cag tcc gtt cca gaa tac gct act  
 66 Asp Asp Cys Asn Val Glu Ile Cys Gln Ser Val Pro Glu Tyr Ala Thr  
 67 110 115 120

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70	Val	Gly	Ser	Pro	Tyr	Pro	Ile	Glu	Ile	Leu	Ala	Ile	Gly	Lys	Lys	Asp	
71	125						130					135					
73	tgt	gtt	gat	gtt	gtg	att	aca	caa	cag	cta	cct	tgc	gaa	gct	gaa	ttc	603
74	Cys	Val	Asp	Val	Val	Ile	Thr	Gln	Gln	Leu	Pro	Cys	Glu	Ala	Glu	Phe	
75	140						145				150		155				
77	gta	agc	agt	gat	cca	gaa	aca	act	cct	aca	agt	gat	ggg	aaa	tta	gtc	651
78	Val	Ser	Ser	Asp	Pro	Glu	Thr	Thr	Pro	Thr	Ser	Asp	Gly	Lys	Leu	Val	
79							160			165			170				
81	tgg	aaa	atc	gat	cgc	ctg	ggt	gca	gga	gat	aaa	tgc	aaa	att	act	gtc	699
82	Trp	Lys	Ile	Asp	Arg	Leu	Gly	Ala	Gly	Asp	Lys	Cys	Lys	Ile	Thr	Val	
83							175			180		185					
85	tgg	gta	aaa	cct	ctt	aaa	gaa	ggt	tgc	tgc	ttc	aca	gct	gct	act	gtc	747
86	Trp	Val	Lys	Pro	Leu	Lys	Glu	Gly	Cys	Cys	Phe	Thr	Ala	Ala	Thr	Val	
87							190			195		200					
89	tgt	gct	tgc	cca	gag	ctc	cgt	tct	tat	act	aaa	tgc	ggt	caa	cca	gcc	795
90	Cys	Ala	Cys	Pro	Glu	Leu	Arg	Ser	Tyr	Thr	Lys	Cys	Gly	Gln	Pro	Ala	
91							205			210		215					
93	att	tgt	att	aag	caa	gaa	gga	cct	gac	tgt	gct	tgc	cta	aga	tgc	cct	843
94	Ile	Cys	Ile	Lys	Gln	Glu	Gly	Pro	Asp	Cys	Ala	Cys	Leu	Arg	Cys	Pro	
95	220						225				230		235				
97	gta	tgc	tac	aaa	atc	gaa	gta	gtg	aac	aca	gga	tct	gct	att	gcc	cgt	891
98	Val	Cys	Tyr	Lys	Ile	Glu	Val	Val	Asn	Thr	Gly	Ser	Ala	Ile	Ala	Arg	
99							240			245		250					
101	aac	gta	act	gta	gat	aat	cct	gtt	ccc	gat	ggc	tat	tct	cat	gca	tct	939
102	Asn	Val	Thr	Val	Asp	Asn	Pro	Val	Pro	Asp	Gly	Tyr	Ser	His	Ala	Ser	
103							255			260		265					
105	ggt	caa	aga	gtt	ctc	tct	ttt	aac	tta	gga	gac	atg	aga	cct	ggc	gat	987
106	Gly	Gln	Arg	Val	Leu	Ser	Phe	Asn	Leu	Gly	Asp	Met	Arg	Pro	Gly	Asp	
107							270			275		280					
109	aaa	aag	gta	ttt	aca	gtt	gag	ttc	tgc	cct	caa	aga	aga	ggt	caa	atc	1035
110	Lys	Lys	Val	Phe	Thr	Val	Glu	Phe	Cys	Pro	Gln	Arg	Arg	Gly	Gln	Ile	
111							285			290		295					
113	act	aac	gtt	gct	act	gta	act	tac	tgc	ggt	gga	cac	aaa	tgt	tct	gca	1083
114	Thr	Asn	Val	Ala	Thr	Val	Thr	Tyr	Cys	Gly	Gly	His	Lys	Cys	Ser	Ala	
115	300						305				310		315				
117	aat	gta	act	aca	gtt	aat	gag	cct	tgt	gta	caa	gta	aat	atc	tct	1131	
118	Asn	Val	Thr	Thr	Val	Val	Asn	Glu	Pro	Cys	Val	Gln	Val	Asn	Ile	Ser	
119							320			325		330					
121	ggt	gct	gat	tgg	tct	tac	gta	tgt	aaa	cct	gtg	gag	tac	tct	atc	tca	1179
122	Gly	Ala	Asp	Trp	Ser	Tyr	Val	Cys	Lys	Pro	Val	Glu	Tyr	Ser	Ile	Ser	
123							335			340		345					
125	gta	tcg	aat	cct	gga	gac	ttg	gtt	ctt	cat	gat	gtc	gtg	atc	caa	gat	1227
126	Val	Ser	Asn	Pro	Gly	Asp	Leu	Val	Leu	His	Asp	Val	Val	Ile	Gln	Asp	
127							350			355		360					
129	aca	ctc	cct	tct	ggt	gtt	aca	gtc	gaa	gct	cct	ggg	gga	gag	atc		1275
130	Thr	Leu	Pro	Ser	Gly	Val	Thr	Val	Leu	Glu	Ala	Pro	Gly	Gly	Glu	Ile	
131							365			370		375					
133	tgc	tgt	aat	aaa	gtt	gtt	tgg	cgt	att	aaa	gaa	atg	tgc	cca	gga	gaa	1323

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137	acc	ctc	cag	ttt	aaa	ctt	gta	gtg	aaa	gct	caa	gtt	cct	gga	aga	ttc	1371
138	Thr	Leu	Gln	Phe	Lys	Leu	Val	Val	Lys	Ala	Gln	Val	Pro	Gly	Arg	Phe	
139						400				405						410	
141	aca	aat	caa	gtt	gca	gta	act	agt	gag	tct	aac	tgc	gga	aca	tgt	aca	1419
142	Thr	Asn	Gln	Val	Ala	Val	Thr	Ser	Glu	Ser	Asn	Cys	Gly	Thr	Cys	Thr	
143					415				420						425		
145	tct	tgc	gca	gaa	aca	aca	aca	cat	tgg	aaa	ggt	ctt	gca	gct	acc	cat	1467
146	Ser	Cys	Ala	Glu	Thr	Thr	His	Trp	Lys	Gly	Leu	Ala	Ala	Thr	His		
147					430				435						440		
149	atg	tgc	gta	tta	gac	aca	aat	gat	cct	atc	tgt	gta	gga	gaa	aat	act	1515
150	Met	Cys	Val	Leu	Asp	Thr	Asn	Asp	Pro	Ile	Cys	Val	Gly	Glu	Asn	Thr	
151					445				450						455		
153	gtc	tat	cgt	atc	tgt	gta	act	aac	cgt	ggt	tct	gct	gaa	gat	act	aac	1563
154	Val	Tyr	Arg	Ile	Cys	Val	Thr	Asn	Arg	Gly	Ser	Ala	Glu	Asp	Thr	Asn	
155					460				465						475		
157	gta	tct	tta	atc	ttg	aag	ttc	tca	aaa	gaa	ctt	cag	cca	ata	gct	tct	1611
158	Val	Ser	Leu	Ile	Leu	Lys	Phe	Ser	Lys	Glu	Leu	Gln	Pro	Ile	Ala	Ser	
159					480				485						490		
161	tca	ggt	cca	act	aaa	gga	acg	att	tca	ggt	aat	acc	gtt	gtt	ttc	gac	1659
162	Ser	Gly	Pro	Thr	Lys	Gly	Thr	Ile	Ser	Gly	Asn	Thr	Val	Val	Phe	Asp	
163					495				500						505		
165	gct	tta	cct	aaa	ctc	ggt	tct	aag	gaa	tct	gta	gag	ttt	tct	gtt	acc	1707
166	Ala	Leu	Pro	Lys	Leu	Gly	Ser	Lys	Glu	Ser	Val	Glu	Phe	Ser	Val	Thr	
167					510				515						520		
169	ttg	aaa	ggt	att	gct	ccc	gga	gat	gct	cgc	ggc	gaa	gct	att	ctt	tct	1755
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171					525				530						535		
173	tct	gat	aca	ctg	act	tca	cca	gta	tca	gac	aca	gaa	aat	acc	cac	gtg	1803
174	Ser	Asp	Thr	Leu	Thr	Ser	Pro	Val	Ser	Asp	Thr	Glu	Asn	Thr	His	Val	
175					540				545						555		
177	tat	taa	attctaa	agg	attatcctaa	agg	agg	gca	tattccgctc	tgcttttagga						1859	
178	Tyr																
180	tagtttcaa	agaagtaccc	tttttagtacc	ttacgtacta	aaggcggttt	tttggtttat										1919	
182	aagcttcca	atccaatcgt	agagtttctt	aatcaaagat	attatctaag	tttctgaaat										1979	
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200	Met	Ala	Ser	Cys	Phe	Ala	Ser	Gly	Gly	Ile	Glu	Ala	Ala	Val	Ala	Glu	
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203	Ser	Leu	Ile	Thr	Lys	Ile	Val	Ala	Ser	Ala	Glu	Thr	Lys	Pro	Ala	Pro	

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212	80		
213	Pro Cys Glu Glu Gly Arg Cys Gln Pro Val Glu Ala Gln Gln Glu Ser		
215	85	90	95
216	Cys Tyr Gly Arg Leu Tyr Ser Val Lys Val Asn Asp Asp Cys Asn Val		
218	100	105	110
219	Glu Ile Cys Gln Ser Val Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr		
221	115	120	125
222	Pro Ile Glu Ile Leu Ala Ile Gly Lys Lys Asp Cys Val Asp Val Val		
224	130	135	140
225	Ile Thr Gln Gln Leu Pro Cys Glu Ala Glu Phe Val Ser Ser Asp Pro		
227	145	150	155
228	160		
230	Glu Thr Thr Pro Thr Ser Asp Gly Lys Leu Val Trp Lys Ile Asp Arg		
231	165	170	175
233	Leu Gly Ala Gly Asp Lys Cys Lys Ile Thr Val Trp Val Lys Pro Leu		
234	180	185	190
236	Lys Glu Gly Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu		
237	195	200	205
239	210	215	220
240	Glu Gly Pro Asp Cys Ala Cys Leu Arg Cys Pro Val Cys Tyr Lys Ile		
242	225	230	235
243	240		
245	Glu Val Val Asn Thr Gly Ser Ala Ile Ala Arg Asn Val Thr Val Asp		
246	245	250	255
248	Asn Pro Val Pro Asp Gly Tyr Ser His Ala Ser Gly Gln Arg Val Leu		
249	260	265	270
251	Ser Phe Asn Leu Gly Asp Met Arg Pro Gly Asp Lys Lys Val Phe Thr		
252	275	280	285
254	Val Glu Phe Cys Pro Gln Arg Arg Gly Gln Ile Thr Asn Val Ala Thr		
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257	295		
260	Val Thr Tyr Cys Gly Gly His Lys Cys Ser Ala Asn Val Thr Thr Val		
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263	320		
266	Val Asn Glu Pro Cys Val Gln Val Asn Ile Ser Gly Ala Asp Trp Ser		
267	325	330	335
269	340	345	350
270	Tyr Val Cys Lys Pro Val Glu Tyr Ser Ile Ser Val Ser Asn Pro Gly		
272	355	360	365
273	365		
275	Val Thr Val Leu Glu Ala Pro Gly Gly Glu Ile Cys Cys Asn Lys Val		
276	370	375	380
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279	Val Trp Arg Ile Lys Glu Met Cys Pro Gly Glu Thr Leu Gln Phe Lys		
280	385	390	395
282	400		
284	Leu Val Val Lys Ala Gln Val Pro Gly Arg Phe Thr Asn Gln Val Ala		
285	405	410	415
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281 Thr Asn Asp Pro Ile Cys Val Gly Glu Asn Thr Val Tyr Arg Ile Cys  
282 450 455 460  
284 Val Thr Asn Arg Gly Ser Ala Glu Asp Thr Asn Val Ser Leu Ile Leu  
285 465 470 475 480  
287 Lys Phe Ser Lys Glu Leu Gln Pro Ile Ala Ser Ser Gly Pro Thr Lys  
288 485 490 495  
290 Gly Thr Ile Ser Gly Asn Thr Val Val Phe Asp Ala Leu Pro Lys Leu  
291 500 505 510  
293 Gly Ser Lys Glu Ser Val Glu Phe Ser Val Thr Leu Lys Gly Ile Ala  
294 515 520 525  
296 Pro Gly Asp Ala Arg Gly Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr  
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**VERIFICATION SUMMARY**

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